

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGTCTTCCCG
CAGCGCTACCGCCATTCGCCTGCCCGCCGGCGCTGGGCTCCTGCCGCTCTGCTG
CTGCTGCCGCCGGAGGCGCCAAGAACGCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAACTTGGCGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCGAGCGACTTCGAATGCAATCAGATGCTAGAGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA
GGGCGACGGGTCTGCCGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTCGAACAGAAAC
GAAGATGCCTGTGCGGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGGCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCCGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATTTGATACTGAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTCTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCGGATCGGAATTAATTGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEARQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQDGSCRHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEEITEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGGTGCCTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGC**ATG**CCCGAGGAGCGCCTTC
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCCACTGCAGGGAGGC
CGGGCCGCCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCTGTCCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTTGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAAACATGTCAACAAGCTGAGTGCCCAGGCCGGTGCAGAACCTCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGTGACTCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAC TGACAAGCAA ACTGCTCAACCACCTGCTTAATGGAGGACC
TGTTTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCCTGCAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTCAAAGCCTGTGCAGCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAAGCCGAGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTATTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTGTTCAGTGCTTGGACAGATTATTTATATTGTCAATTGA
TCAGGTTAAAATTCAGTGCTGAGTGGCAGATATTCTAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCTAGATTATTGTCAAGATATTAGAT
GTTGTTACATTAAAATTGCTCTTAATTCTAAACTCTCAATAACATATTGGACC
TTACCAATTCCAGAGATTCACTTAAACAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAAATAATGTATGAACCTTTGCAT
TGGCTTGAAGCAATATAATATTGTAAACAAAACACAGCTCTACCTAATAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKEALCTPRCMNGGLCVTPGFCICPPGFYGVNCNKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGKSCKCSKGYQGDLCSPVVC
EPGCAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGGTGCAGAGCCAGGAGGCCAGGGCGAGGCCAGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACCATGTGGCGATGCCACTGGGCTAC
TGCTGTTGCTGCCGTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCAGGGAGGCCGTACTGCCAGGA
GCAGGGACCTGTGCTGCCCGGTGCCAGCAGACTGTGCCCTGCCACTTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGGAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCTGAGGGCATTGCCTACCGCCTGGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACTAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGGCTCTGAGAAGTGGCCAACCTGATTGAGCCTTGA
CCAAGGCAACTGTGAGGCTCCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTGATGGTGCTGGTGGTTCTCGCTCG
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGATGAGGACTTCTCCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGG
AGAGGAGACGCTGCCAGATGAAAGGACGCTAAACTGGACTGCGGCCACTCCTGGGCC
CAGCCTGGGCCGAGAGGGCCACTCCGCATCGTGCAGGCCGTCAATGAGTGCACATCGAG
AGCTTCGTGCTGGCGTCTGGGCCCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGATCCAGGCTAAGGGCCGGCGAACAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGGCGCAGGGCGCTAAAT
CCCGCGCGGGTCCGCTGACGCAAGGCCCTGGAGGCCAGGGCTGGGAAGAGCACAGCTGCAG
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGTTCA
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAAGT
CCTGGCTCAAGCGGTCCACCTGCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTTCACTGTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC
ALPYLGAIKYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHQSHQPGQLWLAGWEQPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATACCGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGA~~T~~CTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGA~~A~~CTGCGTGGATGA~~T~~TCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGC~~CC~~CAGGCCTCTGTGCCACTCCTCACAGACCTG
GCC~~C~~AGTGGGAGCCTGTCCTGGTTCTGAGGCACATCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCC~~T~~GACCC~~T~~CCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCGCCTGCAGATGCCCTCCAACCC~~T~~CTGCTGCTGTTTC
CATGCCAGCATTCTCCACCC~~T~~TAACCC~~T~~GTGCTCAGGCACCTCTCCCCAGGAAGC~~TT~~
CCCTGCCACCC~~T~~ATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCAGGACCA~~CC~~CAGCA
GGGGACAGGC~~A~~CTCAGGAGGGCC~~C~~AG~~TAA~~AGGCTGAGATGAAGTGGACTGAGTAGAA~~CT~~GGAA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGC~~T~~GGAGGAA
GGGCCAGGC~~T~~CACATTG~~T~~GGGCTCC~~T~~GAATGGCAGCCTGAGCACAGCGTAGGCC~~TT~~
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCAACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGGAAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGGCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGGCAGGGCGGGCCCGCCAGGCTCCGCAGGCCAGAAC
CAGCGCAGGCCACTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGCAGTTCGAGTTGTGGCTCCGCCCGACCGCCGGACCAAGCGCACAC
GGCGGCCAGGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGGCCCTCCC
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGCAGGCCGGTG
GAGGGAGGACCTGAGGCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGCCCCAGCCCCAAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTAGGAAAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCCACATCCAGT
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACACATTGTATTTAT
TTCCGTACTCAGAA**ATGG**GCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGCCTACTCACAGGTGTCACAGGCTTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGCAAGGAAAAC
AATATTGACACCATTTCACGGGCTGCTTGCCCAGCTTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCAG
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTGGAGCGTCTATTGTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
AGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCGAGAT
AAACACATTCCTTGAACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTTGATAATTCTCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTGACTGCAGTATTAAATGGTCACAGAATGGCTCAA
ATATATCCCTCATCTCTCACGTGGGGTTTCACTGTGCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTCAAGGAATTAAATATGAATTCTTGTCCCTGACCACGACCCCCGGCCTG
CCTCTTCAACCCAGCCCCAAGTACAGCTCTCGACCACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTCCTACACATCGAAACTTCCACGATT
CTGACTGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTCTATC
CATTGTAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTCACCGTGATGGCATA
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGCATCGTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATGGATT
TGTTAGTGCCTGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTAGGAG
CACCAACCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACAGTTCAAGATCGTCTCTTAAATAACGAT
CAAACCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACG**TGAC**CAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRNFVYCNERSLTSVPLGIP~~
EGVT~~VLYLHNNQINNAGFP~~AELHN~~VQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI~~
SRAALAQLLKLEELHLD~~DNSISTVGVEDGAFREAI~~SLKLLFLSKNH~~LSSVPVGLPVDLQELR~~
VDENRIAVI~~SDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLT~~KLKEFSIVRN~~NLSHPPD~~
LP~~GTHLIRILYLDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNL~~SNL~~KQLTARNN~~
PWFCDCSIK~~WVTEWLKYIPSSLNVRGFMCGPEQVRGM~~AVRELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPN~~PSSRSYTPPT~~SKLPTI~~PDWDGRERVTPPISERIQLSIHFVND~~
TSIQVSWL~~SLFTVMAYKLTWVKMGHSLVGGIVQERIVSGE~~KQHLSLVNLEPRSTYR~~ICLVPL~~
DAFN~~YRAVEDTICSEATTHASYLNNGNTASSHEQTTSHSMGS~~P~~FLLAGLIGGAVIFV~~L~~VVL~~
LSVFCWHMHKKGRY~~TSQWKYNRGRRKDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNNDQ~~LLKG
DFRLQ~~PIYTPNGGINYTDCHIPNNMRYCNSSVPDLEH~~CH~~T~~

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCGCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTGGCGAGGCAGAGGCCAGAGGAACACCCGGGCTGGCTCGCCCGCTGCC
TCGCTTCCCAGGCAGGCCGGCTGAGCCTTGCCTCCCTTGCTGCCCTGAAATGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCCCTCCCTGCCAGGGCAGGGCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGGAGACACGCTCGGACCCACCGCAGACGCCCTCTGGAGAGTTCTGTGAGAACACAAGCGGGAGACACC
TGGTTTCATATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTGGACATTGGTCTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCCGATCTGTCCACGG
GCACCATGACTGGCTGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGCTATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCGAGGTGGCTGCTA
AGGCACGGGACACGGGCTTAATCTTGCATTGGCTGTGGCCAGGTAGACTCAACACCTGAAGTCCATTG
GGAGTGGAGCCCCATGAGGACCATGTCCTTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCAACGGCCACATGTGACAGCACCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAAGGCTACATTCTCAACTGGATCAGACAGACTTGAGCAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCAGGTGGCTCTTCGTCAGTGCCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCCCTAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTCCACAAGGATCAACTACTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGCCTAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGAACACACGGAGGATCCCTGCTGCCAGTGCTCAGAAGGCTTC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGAAAGACGTGTG
CAAATTGGACTTTGTCTGGGGGACACGGTTGTGAACATTGTGTAAGCAGTGAAGGATTCGTTGTG
GCCAGTGCTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGAGAAGGAAAGATGCTGCCAGCTATA
ACCATGGCTGTGAACACATTGTGTAACAGTGACGACTCATACAGTGCAGTGCTGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCAGGGAGGATGTCTGCAAATCAACCCACATGGCTGCAACACATTGTGTTA
ATAATTGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAGAAA
GCACGTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTC
TGAAGCAGTTGTCAGTGAATTAGATTAGATTCTTGACAAATTCCCCAAAGCGCTGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCACACAGAGTTCACTCTGAGAAAACCTCAACTCAGGCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAAATACAGGAAAGGGCTCATGACTGGGCTGCCAGGCAACATGGTGAAGGAGGAGTTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTCCCAGACGAGCCATTGTGTTACCGAGGACGGCTCAGGATG
ACGCTCCGAGTGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGTAGGAAAAGCCATTG
AGGAGGAACATCAAGAGATTGCTCTGAGCCACAAACAAGCATCTTCTATGCCAGACTCAGGCAAATGG
ATGAGATAAGTGAAAAACCTCAAGAACAGGATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCAG
CAGGGGAACAGGCAAAACGGTCCAAACAGCCAACAGAACAGAACATTGAGCCAGTCACCATTAATATCCAAGACCTACTT
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAAGCTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTGGAAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCTGAGATACAGATGAAGATTAGAAATCGCAGACATTTGAGTCATTGTATCAGGATTACAAT
GAACGCAGTGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTAAGTAACTTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTTGTAATATACTGTGGACAC
AACTGCTTCTGCCTCATCCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTAATTGTGAGAACAGTTGGATTAAATACAATATTAAACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGHRARTHPTALLESSCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAVKMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAGFCINIPIGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGECHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCALKDSCALGDHGCEHSCVSSEDHFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENFEVVVKQFVTGIIDSЛИSPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDELLRSTQQLSHSTKPSGPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG
GCACCTGCAGGTCCCGTGCCTCCCGCGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGCTGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAACATGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**
CCCACCACTCATTGGCTAAAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCTGGCTCCAGGC
CCCCTGATCTGACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGTTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAGACTAACATGAAATATGTGTTGTTCTATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACNCNTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIAPIRTLPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIP GGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACC GCCA**ATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG**
TTGAATTGTTCTATACTCAA**ATTGACCAAGACACCTGTCTCCAAATGCAAAATGTGA**
AATACGCAATGGAATTGAAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAATTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTACAGAACAAACA
CTATCTAGCCAAGGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTACAAA**ACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTC**
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTCTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGTCAATTGGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTGCTTGCCATATGCATT
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAAATTCAAACAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATAACAAATAACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTGATGGATGTGC
ATTGAAGGCATACATCTCATGTTGTGGGTGTCATCTACAACAAAGGGATTGGCA
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCAGAAACACTTATT
TGGAGTTTATAGGACCAGCATGCCATAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTGTTCTCGGCACCACTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTCCAGGGATGTTCAATTGTTATCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAA**AAATGTCCCCTGTTGGATGTTAAGGTAACATAGAGAATG**
GTGGATAATTACA**ACTGCACAAAATAAAATTCAAAGCTGTGGATGACCAATGTATAAAA**
TGACTCATCAAATTATCCAATTATTAAACTACTAGACAAAAGTATTAAACATTGTTCT
GTTATGCTATAGGA**ACTGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT**
TTTCTATGTGAAATAGTTCTGTC**AAAATAGTATTGCAAGATATTGAAAGTAATTGGTTT**
CTCAGGAGTGA**TATCACTGCACCCAAAGGAAAGATTCTTCTTAACACGAGAAGTATATGAA**
TGTCTGAAGGAA**ACCTGGCTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC**
CCTACCACCTCGGTATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACATGAAGGGCAGA
ATATCAA**ACAGTGAAGGAAAGGAAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC**
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAAGAACACATTACATTGTGAA
TTGTTCTGA**ACTTAAATGTCACAAAACAATTGACTAGACTTCTGTTGCTAAATCTGTTCTT**
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVNANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEVEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFEVKTVNNFVQRDTFVWDKLSVNHRRTHLTLMHTVEQATLRISQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFS AALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCTCCGCAGATCCGAACGGCCTGGGCCGGGTCAACCCGGCTGGGA
CAAGAACGCCGCCCTGCCTGCCGGGCCGGGGAGGGGGCTGGGCTGGGCCGGAGGCCG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGTCAAGCAGGAGCGCTCGCTCAGGATCTAGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTCGGCCAGAGCCCCAGGGAGGTGCCATTCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGCGCCCCCTCGCTTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGCACCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTCCTGCGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGGC
CAGAGCGCCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCAGGTACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACGCCAGCATG
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCACGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCGGCCCCATTCTGCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTTCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTTGCTGTCCGGTGTACCTGC
TTCCATCTCCCAGCCCACCAGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCCTTACCTTATGTCAACCTGCACTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAGATGGCGAGGAGGAGGCCACCGCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCTTAGTGATTCCTGTGGCTTGTGCTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGA~~AA~~ATGTGCAGTGGCTACGCCGTAA~~T~~CCAGCAGTTGGAAAGG
CCGGCGGGCGGATCACGAGGT~~C~~AGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAAATCACTGAACCCGGGAGGCGGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATCTGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGISSLLENPRLGSQST
NSSYTMTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAAVVVA
LVIISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACTGCTCCACAGCCGGACCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTCTATGGCATTCA
TTTGACAAATGCAAGCATTCCCTTATCAATCAGCTCCTATTGAACCTACTGACTGACTG
TGGAACTCCTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCTGAAAAATGTCGTCCGAAC TGAGCAACTTACAAGAACTCTATATTACACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACAGATAACGCTTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATT TAGCAATATGCTACACTAAAGAGTTGGGATAAAATAATGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAAATAGAAC
TACTAACAAACCTAGATTGCTTACATTCAACCCCAATGCATTTTCAGACTCCCCAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTACCGTTG
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGT CAGAATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGT
CTCCCTTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCATTCTGAGGGAAACACTA
GATATAAATGGCGTAACTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTGAACTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAGAGATATTCAAGGCCATTCAAGTTGGTGTGAAAGACTGAAATTCTCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGCAAGACTGAAATTCTCA
TGCTGCCTAAAGTGCCTGAATACCCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTACAGAAAAACAGAAAAAA
TGTGTAATGTCACCAACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAGAATAATAC
CACAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACTGTTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCAATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINRLSLVIAGINLTEIPDNAVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPPELISIDS LAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNAL SALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFM EPDSLFCVDPPEFQGQNV RQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHC RATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTL DINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRD IQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE
YEKNNTT LMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKV KATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAA**CTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT**
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCAGATTGCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**AAGTGTCCAAACTGACTGT**CATTGAGAAAGAAAGAAA
GTAGTTGGCATTGCACTAGAAATAAGTGGTTACTTCTCCATTGAAACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKGCLCSSSGGLNVTC SANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASN HETAHNVI CKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVI SYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGAACCGAAGGCAGGCCGGAGAATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTGGCCACGGCTGCCGCCCCGCTGCGAGTGCCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGTGCTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCACCTGGAGGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCACAAACACTCTCACCTCCGGACGCTGGGTCTCCGAGCAACGCCCTGAAGCTCATC
CCGCTAGGGCTCTTCACTGGCCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTCAGCGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGTGTCCCACCTGCACGCCCT
CATCGTCCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCCGCTTCAACCTCTTACAACCCCCATCA
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCGGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTGGCTCTGTGGGTGTTCCGG
CGCCGCTGGCGCTCAACTCAACCGCAGCAGGCCACGTGCGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCC
CCCGCATCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT
GTGTGCCGGCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCCACACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGAGCTACTGCCGACTGGCCCCATCAGCCAAACAA
GACCTTCGCTTCATCTCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACACCATGGCTCATCTTT
CTGGCGTGTCTCTGCCTGGTGTGCTGTTCTGGAGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCTCCGCAAGTTCAACATGAAGATGATAATGGGCGGGGGGGGGCAGGGACCCCCG
GGCGGCCGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCCTCCACCTC
CTCCCTACCTCTACACACGTTCTTTCTCCCTCCGCCCTCGTCCCTGCTGCC
CCAGCCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELENENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDLMTTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLYLRFLNLSYNPISTIEGSMHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGCACCTGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGC
TGTCGCCTGCTGGCGCCGGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGCTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGAGCATCGTGTGCTCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCAGAAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
AACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGGACACGCCATCATCAATGAGAAGGG
GGCAGTCAGGAGGGGAGCACAAGAAGGAATATTCATCTAGAGGCGCTGCCACTCCTGC
GCCCCCCAGGGGCCGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV
TVLGI P Q K P I I T G Y K S S L R E K D T A T L N C Q S S G S K P A A R L T W R K G D Q E L H G E P T R I Q E D P N G K
T F T V S S S V T F Q V T R E D D G A S I V C S V N H E S L K G A D R S T S Q R I E V L Y T P T A M I R P D P P H P R E G Q
K L L L H C E G R G N P V P Q Q Y L W E K E G S V P P L K M T Q E S A L I F P F L N K S D S G T Y G C T A T S N M G S Y K A
Y Y T L N V N D P S P V P S S S T Y H A I I G G I V A F I V F L L I M L I F L G H Y L I R H K G T Y L T H E A K G S D D
A P D A D T A I I N A E G G Q S G G D D K K E Y F I

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCCTTAAACCCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTCTGGGCTGAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACCTGCCAAC
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCCT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAAGAGACCTTGCTCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCACACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCAGG
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG
CTGAGGTCCCTGCCGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCACGGAAACCCCTGGGAGTGCTCTGCACAAATTGTGCCTTCAAGCAGTGG
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGGGAGACCGGACGCAC
AACTCCTACCTAGACACCAAGCAGGGTGTCCATCTCGGTGTTGGCTCCGGACTGCTGCTGG
GTTGTCACCTCCGCCCTCACCGTGGGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACCTCCCGCGTCCGAGGATTAATTCCCTACAGACAGTCTG
GACTCTCCTACTGGCACAAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAGGG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAFTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLINEETTEQDLCPLKNRVDSSLAPPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LPCPGGCSDHI PGSGLKMNCCNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLTVFTSAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTCTGTCGCGGCCAAGGGAAACTGTTGGC
CGCTGGGCCGGGGGATTCTTGGCAGTTGGGGTCCGTCGGAGCGAGGGCGGAGGG
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCAGACAC
AGCTCTGCGCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCTCCTCTGGCAGGCGCTCTGGCCCGGGCGGCG
CGCGAACACCCCCACTGCCGACCGTGCTGGCTCGGCCTCGGGGCGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGAGGGCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCTGTGCTCGCCTCTGCGGGCAGGCCAGG
GCCGGAGGGGCTCAAAGACCTGCTGTTGGTGCACGGCGTCCCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCCTCCGACCCGGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCGAGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACGGCTACCTGTGCAAGTACCAAGTGTGAGGTCTGTGTCCTGCGCCGCCGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAATGCGCTAGACGACTGGGAGG
CTTGCGCTGGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCCGCTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACGGGGTGCACCAGGCGCCGCCGACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCAAGTAACATCTATTCCGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTGTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTTGGCTCTAGTGATGCATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACATTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGATACTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCAGGGAAAAAATAAAAATTTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWP GP GGG E HPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCGCCGGCGCGCGCCGTGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTAUTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTCCCAGAAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGGATTACCTGCAGGAGTCATTGTGTGGCACATTGTAGCCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCACT
TTTATCAGACTTAAGTTAATGCAACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTTGTGTCACAAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCACACATCTACAAAGAGGGAAATTGGCGATTGAGCAGGGGG
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCCTCAGAACAGGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGGAGGGAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTTAAAAAATAGCAATG
TAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCGTTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAAAAAA

FIGURE 38

MRGANAWPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRTDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGVGEDGRGKIMPNSFIMMFTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAAGCACTCAGACTCGAGTGCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCCCTGGGGAACAGAGAGGCCCTCGGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCAGACTGTGCC
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTCAAAAGTTTCTTAATGGTGGTGCAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCTGGTERPCGGYGCCEGEGRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCASFAGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTACATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCCGTGCACAGGCACGGGCCGTGCTCCCGCGCAGGCCCGGGCC
CGGGTACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCAAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGCGCTCGTGCCTGCCAGGAGGCTCCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGGAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAACCTAATTGGCTCTCAGGAATGAGAATCTTGGCACTGGA
GAGCCCTGCTCAGTTCTATTACTGACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGGCTGGTGTCAAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCAGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACCATGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCGCCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCACAGGGCCCCACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTCGAGGAATCTGACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTGAGCTGGTTCTGGCTTTCCATTGGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATTGGAAAGTG
CCACTGGGATCCCTCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAATTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGGCCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTATGCGTGCCCCCACCTGG
CGCTGCACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCACGGCCA
CCCAGACTGTCCCAGCAGCGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCAGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCAGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTCAAGCCTGGTACCGCCACCCCTCCTTTGTCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCAACTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGCGGATGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNC SRLA CLAGELRCTL SDDCIPLTWRC DGH PDCPDSS DEL GCGTNE ILPEGDATT MGPPVT
LES VTS LRN ATT MGPPVT LES VPS VGNAT SSS AGD QSGS PTAY GVIA AAAA VLS ASL VTAT LL
LL SWL R A Q E RL RPL GL L VAM KES L LL SEQ K TS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGGTCCGGTCTCGCTCGCGCAGCGGGGGCAGCAGAGGTCGCACAGATGCGG
GTTAGACTGGGGGGGGAGGAGGCGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTCAAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCGCACAGCTCACGGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCGAGAATGGCTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTGTGATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTTAAACTT
GATGGGTCTCGTATCTTGAGTGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCACCTACCTCAAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGGCCTTGTGAGCGCTACAACCACCGAACTGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTGGTAGACGGCGTGCCTAGGCCCCGGTACATGGCCTCTGTGGGCCAG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTAGGCCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGGACACGGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTTAAAAAATTCCAAAGTGTGCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTCTCTTGTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSYDKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASNDPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCGCCCTCCCCCGCCTCCGGTGCAGTCGGTCCGTGGCCTAGAGA
TGCTGCTGCCCGGGTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGGCCCGAGTGCGGGGGCGCACCCGAGTCGGGCC**ATG**AGGCCGGAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGCGCTGAGTGCCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACACTTGAGGAAGCCAAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACCTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCATTGCAAATATTCTGATGAGAACCCAGCAGTTCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAACGATGCCAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACCCAGCTAGCACAAAGAACACACCATC
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAACATTTCAATTCCGAGTGTGTT
CGGGAGAACCACTCCGATGACATGTCTTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATT**TAG**GACATATAAAAACGAAACTGACAACAATGGAAAAGAAATGATAAGAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGTTATGAGAACAGCTATGAGCTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCACGTTGGCTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGTTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACACCTCTGGTCTATACAG
CAGCACATATTACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAACATCAAATAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLL
VTTVVVCWWICRKRKREQPDPSDKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCC CGGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTT CAGCATGCGCTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATT CAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACAGAGGCCGGAGGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTTACCAAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCCTGGCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~C~~GG~~TGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACC~~GT~~GATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATA~~C~~ATTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAA~~CC~~AGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCA~~GG~~CTGGCTGACGCCCTGGCATTGCAAGGGAC~~CG~~TGGAAGTGAA
GCACCAGAAC~~CC~~AGTGGTATACC~~GT~~GCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG
TGTGCCGGCAGCTGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACC~~AT~~GATGAAGACACGTGGT~~CG~~
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGACAA~~CC~~CTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACA~~AA~~CTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAGTCCCTCTCCCTC~~TT~~CAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC~~C~~AGCACAGATTTGGGTT~~C~~ACGACTGCA~~CC~~ACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGC~~A~~T~~C~~ATCTAA~~T~~CTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAACAGAAGGGAGCATTACTGTCTACATGACTGC~~A~~TGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAA~~T~~ACTGGCTGCCCTGATTCTCAGGC~~TT~~CAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA~~A~~CTACATCA
CCACCTTCCTATGTC~~C~~ACATTGCACACAGCAGATTCCCAGC~~CC~~ATAATTGTGT~~T~~
CAACTACTAA~~A~~ACATTCTCACACACACACACACACACACACACACACACATA
CACCATTGTC~~C~~CTGTTCTGAAGAA~~C~~TTGACAA~~A~~ACAGATTG~~T~~GTACTGAAAGAGA
TTCTAGAGGAAC~~GG~~AATT~~T~~AAGGATAAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTG~~G~~TAA~~C~~TTATTACAATAATAAGATAGC~~A~~
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTVCQGTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCC**ATG**GACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGGA
TGTGGACAAGAGGGTCAATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAGAGCGGAAATCC
AAGAACTCC**TAGT**ACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGCTCACAAGTGGG
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAI VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTDVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVI LADLLPSLAVYLRT LAPGLFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGG
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTG
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCAGGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCGCTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATAACTGGAGTCAAAACACATG
TCTGTGTCCTAATTGCTAAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAACATG
ATTTTTATTCCATCTTCTATAGCTTTTAACAACATTGAAAGGATCCTTCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAAAGCACCTAGTTCTGAAAATGATTACAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTTACTACCACTTGTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGAA
AATTGTACCATAACGTTATTAAACATATATTATTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTTCACAATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGTACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAAAAAA
AAAAAAA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKS
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHSVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCCACCGCGTCCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTGGTGGCATGTGGAAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGCTGTTCGCTCCCTACAGAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TCCCAGCTCAGATACAGCAGAAGATGCCAGTAGTTCTGGTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTCCCTGGACCACAACGCTCTCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATACCCACGGATATGCACTGAGGACGATGT
AGCACGGGATTTATAACAGTGCACTAATTCACTAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCATTGCACACCTC
ATCCATTCCCTCAACCCGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACGAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACCTGGTTGAGGCCTTGAATACTGGATAAACTACTAGATGGCACTAAC
AAGTGAACCTTACTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTCGACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCCATGGTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAAATGCCAACACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGGAAAGGATCCAGGAATACAAGAAGGAGAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGGGTGACTTCCATCAGGTAAATTATTC
GAGGTGGAGGACATATTTCACCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCTTGTGAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTGAAACAAGTGGC
TTTGTGTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGCTTGAATAGGAAGTTAATTCTCTAAGAGTAAGTGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL
VGPFPGNMKSYAGFLTVDKTYNSNLFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
TTTCCCTTCCTAACAAAGTTCTAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATCCTAACAGGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGT
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTGTGGCTCTCAGTGGCTGGGTCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCACGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGAGCCCTGAGCGAAGTGCTCACCTCACCAACAATGTCACAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTTACCCAGGGGTCTGCA
AGCTGCTGCGCTGGATGACCTCTTACATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTGTGAGGTGAGGA
TGGCAAGCTTCTCATCGGACGGCTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAGCTGCCGAGACCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTTCACTCATACGTGTCCCTGCCCTCGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGAGGCTGCTTACCTGCCAACGCTGGGACTCACTGGCC
AGGCCTCAATATCACAGCCAGGACGTACTCTTGCCATCTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCGATGACTCTGCCCTGTGTCCTCCCTATCCGGGCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCCTGCTACCGGGCAGGGCACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGACCGAAGGCCCTGCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCAGTTACAACGGCTACAGCGTGGTTTG
TGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGCTCAATGCC
ATTACCTCCTCAGCAAAGAGTCCCTTGGAAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTGTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCCAAACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTNFNHLTVHQGTGAVYVGAINRV
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLI IDYSENRLLAGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMGYGVI VRSEGEGDKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFA SGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL AQA FNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKE SLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGGGCTGAGTGGACTGGAAACCGGGCCCCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCGCGGAGGCCGGCCGCACGCTGGACTCCTGCTGGTCTTGGGCTCTGGTGCCTC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCGTGCCCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGGGCTTGACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTCTGGAAACCTGGACCTGGAGGCCCTCGTCTGATGGCGCAGAGATCG
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTGCCCAGCTGGCTAC
TCCAAGACCTGGCATGAGGCTGAGGACAACTTACAAGGGCTTCACCGAAGCAGTGGACCTTATTGACCACC
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGCTGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTT CCTATAATAAAGACCCGCATACATGCCCTACGTCAAGAAGGACTGGAGGACCGTGGCATTGGAACTGC
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCACT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCCAGGGACTCAGGCCAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTTGGATTCTGAGGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGACCCAACCTTGCTCATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCACAGCTATGACTATGATGCTGTGACAGAACGGCG
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCCTCCCCCACCTG
ACCTTCTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATGCAACTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTATGAGGACCGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG
TGTGGTGAACACAGTACATGAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGGAGGATCTGGTGGAGAATCGTGGGAGTCAGTCAACTATGGGAGAATATTGATGACCAGCGAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCTGAGGAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNGTTCCCTCCAGAAAACACCCACATTACCTGTTCTTCTGG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA
TCAATGGCCAGAACCTGGACTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGCGGGCCCTGCATTACAGTTACGGAAACCCCCC
ACCTGGGAGGAACCAAGTACATTAAGTGAGGGTGGCACCCCTCTGGTGCAGTGGGAGACTGCCCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAAGCTGCAGGGAAAGGTGGATGGCTCTGGGCC
TGGTTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCGGAGGCTGTGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAGTGTGAAACGTGCCCTGCACCGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTTGCTGGTCTGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCCTCACAACCTCTGAGCCTCTTGGATTCTGAAGGAACTCGGCGTGGAGAAACATGTGACTTCCCTT
TCCCTTCCACTCGCTCTCCACAGGTGACAGGCTGGCTGGAGAAAACAGAAACATCTCACCCCTGGCTCTTCC
CAAGTTAGCAGGTGTCTGGTCTGGTCAAGTGAGGAGGACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
CATCCAGGGAGGAGCACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCACATCC
AGGGAGGAGGAGCACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCACATCCAGGG
GGAGGAGAACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCACATCCAGGGAGGAGG
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGAGCAGGCCCTCTTC
GAAGTGTGTCCAAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTGGCTACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PART LG LLLL VV LG FL VL RR LD WST LV P L R LR QL GL QAK GWN F M L E D S T FW
I FGG SI HY F R V P REY W R DR LL K MK A C G L N T L T T Y V P W N L H E P E R G K F D F S G N L D L E A F V L M A
A E I G L W V I L R P G P Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V L A T
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**
AAGAAGCTGTCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTGCTAGTGGATAGGGTCATGACCGGTTCTCTAGACGGGGCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTGCTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGCTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCATTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GACTCTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCTGTT
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGAGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCCTGGATTACTACCAAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCCTAGACTTGCTTGGCCCCGTGGCCCAT
TCATTCAATCTTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTTGTGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGAGCGAACATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGTTGGGTCTAACAGCAGTGAACCTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATCCTGCTGTTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAAGCTGATAACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACT**TGAAAGGTAGGCCGGCATGGCTCATGC**
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACCTCCAGCCTGGCTACAGTGA
GACACTCCATCTAAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRS FVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRA LLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYE PHGPLVNSEYYTGWL DYWGQNHS TRSVSAVTKGLENMLKGASVN MYMFHG GTNF
GYWNGADKKGRFLPITT SYDYD APISEAGDPTPKLFAL RDVISK QEVPLGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTH TIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLT GKLGSKLDILVENMGRLSFGSNSSDFKG LLKP
PILGQTILTQWMMFPLKIDNLVKWFWPLQLPKWPYPQAPSGPTFYSKTFFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCATGTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTCAGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT
GCCTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTCACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTTGCTCAAAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTAACATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG
TGGAAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTAAGTCATTCAAATCATTGTTTTAAATTGTTGTAACCTGGAT
AAAGGGAAAGGAAAATTATAACTAAATCTTGGTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGKLLVLSLKKMMNVAELELQNCELERIPHAI FSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCATTCCATTCTTCATTGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGAAAGACATTGTGTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGCATTGCTTAGTGGTTGTGAGGGAGGACACGTGG
GCTCAGTGCTTGCTGCACCTATGCCTAGGTACATGAAGTCTTGACCTACAGTGAATTGCTGTC
ATCGCTGGTGGTACCTGGCCTGCTCCGTGATAGTTGCTGCTGTCTTACTTCAAACACAAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGGCTGTAAAAAATCACACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCATTGCCACGGAGCTGTGCTGCCCTGCAGTGCTGAAGGATATAGAATGTGTC
AGTTTGATTCCCTGCCACCTTGCTGCTGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCACAGAAAGGACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTTCAGGAAGGAGTTGGGAGAGAACCCTCACTGTGGGAATGCTGATAAACAGTC
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGACTGACGTTCCCTGGAGGTGTCAGAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCTCTAAGGCTGCCAGGCCCTGCCAAA**ATGAGCTGTA**
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGGGAGCTGACAATGGGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCAATATGGCAGAGACCAAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGCAGAAAACAAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGAAAGCTGAAAGTAAAACATTAAGTCTTGACGGAACCTCAGCAATGGGCCTGCTGAGGG
CAAGTCTGCAAGTAAAACGACTATGTCCTGATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGCTTTCTACTACTTCTCTCTCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAAGGATCCTTCACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGTTAT
TGTGTTGTCACATACAAGTGGAGAAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTTCGAATCGTCAACTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTCCTACACCTCAATTATGCAAGAAACATCAACACTACATCTTAACTTGCTCTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTTAACTCTAACTGAAACTTGCAACTAAA
GACCCAACCTGCAAGACAAAATTATCAAATGTTGGAATTCTGCTCCCTCTAATGGATGTTACAATCAGA
AAGGTAGAAGATCAGTCAATTACACCAATATAATCACCTTCTGCATCTCAACTCTGAAGTGTACCC
CGTCAGAAACAACCTCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATAACACCGCATGGCTTTTGAACTTCAATTCTGCA
TTTGGAAAAGACTATACTTGAAATCACCATTATGTGGATTGAACTCTTGTCAAGTTAGTCTGCAC
ACCTCAGATCAAATTGTTGTTCTGATACCTGTAAGGCCCTCTCCACCTCTGACTTGCATCTCAAACC
TACGACCTAATCAAGAGTGGATGTAAGTGCAGAGTGAAACTGTAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAACTGCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGACCAACAGTCTGCTGCAATCAAGGTTGTCCTCAGAAGCAACAGGACACTTCTCATATAATGG
AAAACAGATTCCATCATGGACCCATTGCTGAAAAGGGATGCAAGTGCAGTGGCAATTCAAGGATTTGAGCAT
GAAACACATGCCAGAAACTCAAACCGCCCTCAACAGTGTGCATCTGTTCTCATGGTTAGCTCTG
AATGTGGTGAACAGTGTAGCGACAATCAGTGAGGCATTGAAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTATT**AA**ACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGTCACCTCGT
GGCTACACATATTGAAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCATGTA

FIGURE 70

MELVRRLMPLTLLILSCLAELETMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSPVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYWKTDIIGPIRLKDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGGACAGCCGGCTGCGCCG
GGAC**ATG**CGGCCCAAGGAGCTCCCAGGCTCGCGTCCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCCTCGACCCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCGCCCAGCTCGTAGCGAGTGGTCTGGTGGATTGGCAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCAGTTCAAATATGAAGAT
TTGGACCACTATTACAGAAAATTTTAATGCCAACAGTGGGAGATATTTCAGGC
CTCTGGTGCCTAACATTCAGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTGTGGAACGGAAATGCCATAGATGAGGGCCAAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACCTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTCCAG
TTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA
CATAAATGGAAAAGTCATGACAATAGACAAACTGTCTGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTACAAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC TG
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATC**TAA**AGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTTCCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACGTGAAATTATGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTAGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATCTGTAAAATGGTCACCTGTATAGGGCACTTACCAAGCAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYEFMKDNYPFSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSPKPEKLVYAIIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCAAGGCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCAAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACCGAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTGTCACTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATGAT
ACTTGGACTAACTCGCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATAACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCC
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCGAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACGAAAGTCCACCC
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAC
CCTCTCCTTATTGTAACCCCTGTCTGATCCTATCCTCCTACCTCCAAAGCTCC
TTTCTAGCCTGGCTATGCTTAATAATATCCACTGGAGAAAGGAGTTTGCAAAGTGAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTGAAAGAGAACACGTATCCACCTGACATGCTCTTGAGGCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTGTTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAAATAAAACTCTTATAAATTCTATTCTATGTA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCT
GTTTGATATTCTAGCTTACTCTCAAACATAATTCTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACACACCAAG
TACATTGTTACCTCTATACCAAGCACATTAAAAGTGCCTTAACAAATGTACT
GCCCTCCTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVISRISPNNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAALKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGGTCTGGCACCTCTAATTGCTCTCGTGTATCGTGCCTGCCGACTTCACGATGG
CTCGCCCAACCTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTAACCCCCACCACAGTGTCA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGCCAAGCTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCAAGGACTCTGCTTCAAGCCCTCTGGCTTGTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTGAGACTTCCTTGTGGTAGGACTGGAGGAGAAACCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDI RMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNI PEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTTAGCCGTCAGGAGCTGCCTGGGACGTTGCCCTGG
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGGCTGTCCTGGTCCA
TTGCTCTGCTGCCGGCTCCTACGGACTGCCCTTACAACGGCTCTACTACTCCA
CGCCAACGACCAGAACCTAGGCAACGGTATGGCAAAGACCTCCTTAATGGAGTGAA
TGGTGGAGACACCCGAGGGAGACCCGTTCACCTACCAAGGGCCAGTGTGATCCTGCC
CGCTACCGCTACGAGCCGGCCTGGCTCCCCGGCGTGTGCGTCAAATGGTGAAGCT
GTCGGAGAACGGGCCCCAGAGAAGGACGTGCTGGCTGCCATGGCTGAGGCACCGC
TTGGGACTACCAAGGCCGCGTGCACCTCGGCAGGACAAAGAGCATGACGTCGCTGG
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGG
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGTGTGGCTTACCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCAGCAGGTCTGTGCAGAGCAGGCTGCC
GTGGCCTCTTGAGCAGCTTCCGGGCTGGAGGAGGGCTGGACTGGTCAACGCC
CTGGCTGCAGGATGCTACGGTGCAGTACCCATCATGTTGCCCGGCAGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCACCG
GTATTCTGCTTCGCTACTGCCCTCAAGGGGGGTGTACTACCTGGAGCACCTGAG
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCC
AGCTCTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCAGCCTGGCTGGCAG
GGCAGCGTCCGCTACCCGTGGTTCACCCGATCCTAACTGTGGCCCCCAGAGC
CCGAAGCTTGCGTCCCCGACCCGAGAGCCCTGTACGGTGTACTGCTACC
ACTAGGACCTGGGCCCTCCCGCCATTCCCTACTGGCTGTATTTATTGAG
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAA
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCAATGCC
GATGCCCACTCCAGGAATCATGCTTGCCTCCCTGGCCATTGCG
GAGGGTCCCCGCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGG
CACAGTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCTCGGAGCTGG
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCC
GCCAGTTCTAGGCTCCAGGC
TCCCTCTGGTCAAAGAATCTGTTGTCATTGTTCT
GGAGGGCCCTCAGGTGTGTACTTG
GGACAATAAATGGTGTATGACTGCC
AAAAAAA
AAAAAAA

FIGURE 78

MGLLLLVPLLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**A**TGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGAC
GGCGACGGCTGGGTGCGCTGGCCAGCTCGCGTGGATCGCGCACACGCAGCAGCGGA
CATACGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCCCTGGGTGAAGAATTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGCTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCAGCCTGGGAGGA
GGAGCCGGCGTGGTGAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGGCCACTGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCT**G**AGCACCGCGCACGCCAGCCTCAGAGGCCCG
CACAATGACGGAGGAGGGCCGCTGGTCTGGCCCCCTCCCTGCCAGGCCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCTGTCACACCCCCAACCCCAAGGGAGGGCTGTGTCAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GC GGCGGGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCTGTCGTTGGCGCCCCGCCTCCCGCGGTGCAGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCGCGAGGCAGCTCCAGACCTAGAGGGCGCTGGCTGGAGCAG
CGGGTCGTCTGTCTCTCTCGGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCAGGGCCTCCGCACCCCTGGCCTGCCGATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTAGGGGACCTGTACGAGTCTATAAGCCTACC
TGGTCGAGAAAACATTCCCTAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACTAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAGATTGAAAGCAGACATTGCATTCTGATTGATGGAGCTTAAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCAAAGTGGTGGTATTATTGATGGTGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACACATGCCAACTGGTTGGCACCAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGGCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGTTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTCTGCAACTAGAATCAGATAACAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTTCTGGTTACAATTACAGTGT
ACTTGTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAAACCTAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRNFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNFIIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCGCACCGCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGAACTCGGTCCAGTCG
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGCCACCTGCTGTGCCTGC
TGCTGGCGCGGGCTCCACGGCCCCCGCGCCGCTCCGACGGCAGCTCGGCTCCAGTC
AAGCCGGCCGGCTCTCAGTACCCGCAGGAGGAGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATGCCATGTCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGAGACGAAGAAGGAGCAGAGGAGCAGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAUTGCCAGTTGCCAGCTCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTGTGCCAGTGGCTCCTGCAAGCCCCACAGCCACAGCCTG
GTGTATGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTCATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCT
GCACTGCTGGAGGGAAAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCCCTACA
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTTGCCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGAGTTCTTCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCAT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGATTTTCTTGAGGCATGCACATCTGGAATTAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATAAGGTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCACCAACAGTGGAGAAAATCAAACCGAGCAGGGCTGTTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACAGTTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAACTCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCTGCCATTACCTCTGCAGCTCTGGCTTGAGTCAAAAACATGGGAGGG
CCAGGCACGGTCACTCACACCTGTAATCCCAGCATTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGCCCTGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGGCCAGGAGAATCGCTGTAATCCAGGAGGCCAGGATGCAGT
CAGCTGAGTGCACCGCTGCACCTCCAGCCTGGTACAGAATGAGACTCTGTCTCAAACAAACACACGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCTTAACCTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCGCTG
GCAATGACTGAGCAGGCCAGAGGACAGGAAAGGAGGATATTGAGGAGGCCAAGAAGTGAACGCCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTTGCTGACCTTACCCCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCTTGTAATGGTCCCTGCCACTGTGCCCCGGTACCCCTGGCATGTTCCCTGCC
ACTCTTGCTAGCTGGGTGGCTGGCCACTGCCACTGTGCCCCGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTCCTACCGCAGGCTACCCACTGTGGACTGCAATGA
CCTATTCCCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTG
CCGTGAGGACAGTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACAGCTTGAGGGCTGCCAGGCTACAGGAACCTATCTCAACACACACCAGCTACCGC
CCCCAGGGCCTTCTGCCCTCAGCAACTTGTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGACTCATGATTGGCGCAACAGGTAGATGCCATCTGGACAT
GAACCTCCGGCCCTGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCTGGAGAGCCTCTCTATGACAACCAAGCTGCCGGGTGCCAGGGC
GGAACAGGTGCCGGCTCAAGTTCTAGACCTCAACAAGAACCCCTCAGGGTAGGGCGGGACTTGC
CAACATGCTGACCTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCC
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGTCTTCCATCCACCCCGCGC
CCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAAACACGCTCTCAGTGCCTGCACAGCAGGGTGGAGTC
CCTGCCAACCTGCAGGGTAGGTAGGTCTCCACGGCAACCCATCCGGCTGTGACTGTCTCCAGC
CACGGGACCCGGTCTCATCGAGCGCAATCCACCCCTGTGCGGAGCCTCCAGCAGGGCT
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCAGGAAGCT
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTCTGCATTGCCGGCACTGGCGAACCCGAACCC
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAGGGTACCCGGTGTACCC
GGAGCTGCCAGGGTAGCAGCAGAACAGGGCTATAACCTGTGTTGCCAGAACCTGGTGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGCCGTCTCCTCCAGCCAGGCAGGGAGGAAGGACAGGGCTGGAGCTCG
GGTCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTCAACCCACCCAGTGTCC
CTGGTCCAGTGCCTCTCCCTCCGGGCCAGGGGCCAGCTCTGGCCCTGCCTCGGG
CAACATTACCCGCTCCTCAGGCCACGGAGTACTGGGCTGCCGTCAAGTGGC
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTCTTGCCACAGAGC
GGCCATCCTGGCTCTGCTGTCTCTGGCAGCTGGCTAGGGCCACCTTGG
GGGTGTGGGTGGAGGCGGCCTCTCCCTCAGCCTGGCTTCTGGGCTGGAGT
GTCTGCTCCCTCGTCCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAG
ACCATTGTCTCAAATTCTGAAAGCTCAGCCTGTTCTCAGCAGTAGAG
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAGGACATGG
CAAGACAGATGGGCTTGTGGCCCTGGGGTCTGCAGCCTG
CCTCTGCTGCCAATTCTGAGGAACATCTCAAGGAACAG
CTCAGTGTGCTCTGGCTGCCCTGGCTTCTG
TCTTCTGCTGACTGCTGCTCTGGCTTCTG
CTCGGGGGCTGCCCTCAATGTGGAGTGA
CGCCCTCATCTCAGCAGCCTGGCTGGCATT
ATGTGTCACCTCCCCAACCGATTCA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGKLFDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMELTMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGDADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPNPTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRRLPPAWFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGCCACACTCTCAAGATCCTGGCGTCCTCTACATCAGCCTAGTCATCTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAAATACGACCCGCTACTCCAA
GCGCTTCGCGCTTCTCTCGGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTACCAAGAACCGCAGGACAAGCTGGAGCTGACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCAGCTGACCATCCCGCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTTACACAGCGGCCAAGATTGAAGCGCTGCGCT
GGCCTTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAACGAGCAAGCTGCCACAGGTGGTCA
AGATGTGGCGTGCACCTGCAGAACGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCCTTCAGCTCAGCCT
CCACAACCTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGGCCCTCTACCTGAACCCAGAACAGATCGAGAACAGATCCCCACCCAGCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACACCTGAGACGCTCCCTCCGGACATCGGCTCCTGCGAGAACCTCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCGGG
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCAGGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCCTCAGGCCGGAGGGGAGGCCAGCTAGCTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGGAGCCCTGGGCCGTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTCTCCCTCTGAGACTCAGTCCCCCAGGGCAAGTGTGTTGGAGGA
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCCTCCCTGGAGGCCAGCTGCCCCAGGGCTGAG
CTGCCACCAGAGGTCTGGACCTCACTTTAGTTCTGGTATTATTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCAAGAAAGTTAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTCCCC
TTGTCCTTATTAGCGATGCCGCCGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGGCGAACAG
CCATGGGACGGTCACCCAGCAGTGCCGGCTGGCTCTCGGGTGCAGTCACGGGAGAGCAGGCCAGCTGGA
AAGGCCAGGCCCTGGAGCTGCTCTCAGTTTTGTGGCAGTTAGTTAGTTTTGTGTTTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGGAAAATGGATGGTTGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCTTCTGGGGAGGGAGGTTTTGTGTTGGGTTTTGGGTTTTGGTGTCTGTTCTTCTCCTC
CTATTGTTCTGGCAGGCACTCATTTCTGTGGCTGTCGGCCAGGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ATCGGGTTGGCTAATCCCCGGATGAAACGGTGCTCCATTGCACCTCCCTCCTGCGCTGCCCTGCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCCTGCCAGGGTGT
CCAGTGCCACCGCTGCCCTCGCTTCCATCAGCCCTGCGCACCTGGTCTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGGCCAGGGCAGGGTGGCTGGTCCAAGCCGGTCCCTGGCCGC
CTGGAGTGACACAGGCCAGTGGCACCTGGTGGCTGGAGGCCAACCTGCTTAGATCACTGGGTCCCCACCT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCGTCCATTGTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTI IKVIKFILII CYTVYYVHN IKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLRQRLTKNAQDKLELHLMGLSGIPDTVFVLDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENRLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCAGGGGT
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTCGAACGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTGACATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTT
TACTGGATTCTGAAAGCTGGTCATATGGTTCCCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTCAAGCAAGAATTAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLGlnAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTGSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGGGGAGAGGAGGCCATGGCGCGCGGGGGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGAGGCCGAACTCGGCGTTGGCGTGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTAAGCTGCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTCGGTGACTCAGGTGGACCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTTGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGGCTCCGGGACCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCGGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGANGCCATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTCCGCCAACCTCCCTGCCCTCAG
CCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACGCCACATCCAGTTACTTCATG
CAGTGGCGTGCCTACCCAGATGTGGCTGACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCTCTGGCTTCTCAACCCAAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGTTGAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCCTACTTAGCTCCAGGTCTTAACCTCTCTG
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGAGATTGCTTCTCAGTTACTCATGTTCTGACCTGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEFLQWML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGGCTGCTCGGCGCGAACAGTGTCTGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC
GCCTGCATAACCGCCTCCCTGTCGTCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTTCATGTGGACCCCAGTGTCTAAGGGAAC
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAACGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTGGGAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGCAGGAAATTATTGGCATTTCAGG
GCACCACTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCCTGGCAGCAATTAGGGTCTCATGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTGT
CAAACTTGATTTATTCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDPLLNPFSTSVKLSTGCTGTLVAEKHVLTA
AAHCIHDGKTYVK
TQKLRVGFLPKFKDGGRGANDSTS
SAMPEQMFKQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFS
GHQWDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGTCTCTCGAGCCTGCTGCCGTCCCCCCCCACCAAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACC GGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGAGC
GGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGTCTACATCAGCCTCTCGCGACCGCTCTGGGTGGAGAAGATCGTCAAGGGTGCA
GCTCCCGGGCGCCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCCGCGCTCCTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTCGGGCGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCTGCCACATATCTTATTATTCCCTCCAATTCAATAAATTATTTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGGAGTC
GGCTGTGGTTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCCTCCAATGTCCCTCTGGCTACCAACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCCTGCCAGGTGAGGCTCAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCA GCTGTGCTCCTGTCA TCTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCGCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTT
TTTGAGTGGGGAGGCAGGGACGAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGNKMERGRGENLFAITDEGMDVPLAMEEWHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAAELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTA ACT GAG TCA GGG CTT TCA TGG GAG CCG CTC AAG AGA ATT CGG TCA TT CCA AGT T **A T G G T G G A C G T**
ACT TCT GTT GTT CT C C C T G C T T G C T T T C A C A T T A G C A G A C C G G A C T T A A G T C A C A C A G A T T A T C T T C A T
C A A G G C A A G T C C A T G A G C C A C C T C A A A G C C T C G A G A A G T G A A C T G A A C A C A A T G A A T T G G A G A C C A T T C C
A A A T C T G G G A C C A G T C T C G G C A A A T A T T A C A C T T C T C C T G G C T G G A A C A C G G A T T G T G A A A T A C T C C C T G A
A C A T C T G A A A G A G T T C A G T C C C T G A A A C T T G G A C C T T A G C A G C A A C A A T T T C A G A G C T C C A A C T G C A T T
T C C A G C C C T A C A G C T C A A A T A T C T G T A T C T C A A C A G C A C C G A T C A C T C A G C T A T C C C A C C C A A G A T G T T A A A C T
T T T G G C C A A C A C A C T C C T G T G T A A A G C T G A A C A C G G A A A C A A G T A A A A T G T A G A T G G A C T G A C T T C C A A G G C C T T G G
G C C C C A A C T G C A A C A T C T C G A A T T G A A C C G A A A C A A G A T T A A A A T G T A G A T G G A C T G A C A T T C C A A G G C C T T G G
T G C T C T G A A G T C T C T G A A A A T G C A A A G G A A A C A C G G A A A C A C G G A A A C A A C A A T A C
C A T G G A A A T T T G C A G T G G A C C A T A C A A C C T A A C A G A G A T T C C A G G A T T C C A G G A C C T T A C G G C T T G G G G G C T T C A G
C A T G G A A A T T T G C A G T G G A C C A T A C A A C C T A A C A G A G A T T C C A G G A C C T T A C G G C T T G G G G G C T T C A G
G C A G G A C C T T A C G G C T T G G A C C A T A C A A C C T A A C A G A G A T T C C A G G A C C T T A C G G C T T G G G G G C T T C A G
T C A G A G C T T T G T A A A T G C C A G T T G T G C C C A T C C T C A G C T G C T A A A A G G A A G A C G A T T T T G C T G T T A G C C A G A
T G G C T T T G T G T G A T G A T T T C C C A A A C C C C A G A T C A C G G T C A G C C A G G A A A C A C G T C G G C A A T A A A A G G T C
C A A T T T G A G T T T C A T C T G C T C A G C T G C C A G C A G T G A T T T C C C C A A T G A C T T T G C T G T G A A A A A G G A C A A T G A
A C T A T G C A T G A T G C T G A A A T G G G A A A T T A T G C A C A C C T C C G G G C C C A A G G T G G C G A G G T G A T G G A G T A T A C C A C
C A T C C T C G G G T C G G G G A G G T G G A A A T T T G C C A G T G A G G G G A A A T A T C A G T G T G C A T C T C C A A T C A C T T G G T C
A T C C T A C T C T G C A A A G C C A A G C T T A C A G T A A A T A T G C T T C C C T C A T T C A C C A A G A C C C C A T G G A T T C C A C C A T
C C G A G C T G G G G C A T G G C A C G C T T G G A G T G T G C T G C T G G G G C A C C C A G G C C C C A G A T A G C C T G G C A G A A G G A
T G G G G G C A C A G A C T T C C C A G C T G C A C G G G A G A G A C G C A T G C A T G T G A T G C C C G A G G A T G A C G T G T T C T T A T C G T
G G A T G T G A A G A T A G A G G A C A T T G G G G T A T A C A G C T G C A C A G C T C A G A A C A G T G C A G G A A G T A T T C A G C A A A T G C
A A C T C T G A C T G C C T A G A A C A C C A T C A T T T T G C G G C C A C T G T G G A C C G A A C T G T A C C A A G G G A G A A C A G C
C G T C C T A C A G T G C A T T G C T G G A G G A A G C C C T C C C C T A A A C T G A A C T G G A C C A A A G A T G A T A G C C C A T T G G T G G T
A A C C G A G A G G A C A T T T T G C A G C A G G C A A T C A G C T T C G A T T A T T G G A C T C A G A T G T C A G T G A T G C T G G G A A
A T A C A C A T G T G A G A T G T C T A A C A C C C T G G C A C T G A G A G A G G A A A C G T G C G C C T C A G T G T G A T C C C A C T C C A A C
C T G C G A C T C C C C T C A G A T G A C A G C C C C A T C G T T A G A C G A T G A C G G A T G G G C C A C T G T G G G T G T C G T G A T C A T A G C
C G T G G T T T G C T G T G G G C A C G T C A C T C G T G T G G G T C A T C A T A T A C C A C A A G G C G G A G G A A T G A A G A
T T G C A G C A T T A C C A A C A C A G A T G A G A C C A A C T T G C C A G C A G A T A T T C C T A G T T A T T G C A T C T C A G G G A A C G T T
A G C T G A C A G G C A G G A T G G G T A C G T G T C T T C A G A A A A G T G G A A G C C A C C A C C A G T T T G T C A C A T C T C A G G T G C T G G
A T T T T T C T T A C C A A C A C A T G A C A G T A G T G G G A C C T G C C A T A T T G A C A A T A T G C A G T G A A G C T G A T G T G G A A G C T G C
C A C A G A T C T G T C T T G C C G T T T T G G G A A C C A G G C C T A T G T A T T T G A A G G G A A A T G T G T A T G G C T C A G A
T C C T T T G A A A C A T A T C A C A G G T T G C A G T C C T G A C C A A G A A C A G T T T A A T G G A C C A T A T G A G C C C A G T T A
C A T A A A G A A A A A G G A G T G C T A C C C A T G T T C T C A T C C T C A G A A G A A T C C T G C G A A C G G A G C T T C A G T A A T A T C
G T G G C C T T C A C A T G T G A G G A A G C T A C T T A A C A C T A G T T A C T C T C A C A A T G A A G G A C C T G G A A T G A A A A A T C T G T G
T C T A A A C A G T C C T C T T A G A T T T T A G T G C A A A T C C A G A G C C A G C G T C G G T T G C C T C G A G T A A T T C T T C A T G G G
T A C C T T T G G A A A A G G C T C T C A G G A G A C C T C A C C T A G A T G C C T A T T C A A G C T T T G G A C A G C C A T C A G A T T G T C A G C C
A A G A G C C T T T A T T T G A A A G G C T C A T T C T C C C A G A C T T G G A C T C T G G G T C A G A G G A A G A T G G G A A A G G A C
A G A T T T C A G G A A G A A A A T C A C A T T T G T A C C T T A A A C A G A C T T T A G A A A A C T A C A G G A C T C C A A A T T T C A G T C
T T A T G A C T T G G A C A C A T A G A C T G A A T G A G A C C A A A G G A A A A G C T T A A C A T A C C T C A A G T G A A C T T T T A T T T A
A A A G A G A G A G A A T C T T A T G T T T T A A T G G A G T T A T G A A T T T T A A A G G A T A A A A T G C T T T A T T T A T A C A G A T
G A A C C A A A A T T A C A A A A G T T A T G A A A A T T T T A T C G G G A A T G A T G C T C A T A A G A A T A C C T T T T A A A C T A
T T T T T T A A C T T T G T T T A T G C A A A A A G T A T C T T A C G T A A A T T A G T A T A A T C A T G A T T A T T T T A T G T A T T
T T A T A T G C C A G A T T T C T T T T A T G G A A A A T G A G T T A C T A A A G C A T T T A A A T A A C C T G C C T T G T A C C A T T T
T T A A A T A G A A G T T A C T C A T T A T T T G C A C A T T A T T T A A A T A A T G T G C A A T T T G A A

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAGQ
GEVMEYTTIQLREREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTER
HFFAAGNQLLIIVDSDVS DAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQM TAPS LDDDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTTLAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCCGGGGGTTGGTGTGTTCTGACATAAATAAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAAC
GGTGTGGTGGTTCTTCTTTGAAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAA
TTTCAGAGAAGAAAAGTGTACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGAGCTGGATTTCTCATCAACCTCCTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTTAACCACCTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCTGCAGCAA
CCAGTTCAAGCAAGGTGATTGTGTTGGAAAAACCTGCGTGGAGGTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGCTTGAGGCACATTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGGCTTTCAATGGTCTGGGAACCTCAACACTCTGGA
ACTCTTGACAAATCGTCTTACTACCAACATTCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGGT
GGCAAACAACCCATTGAAAGCATCCCTTCTATGCTTTAACAGAAATTCTCTTGCCTGACTAGACTTAGG
GGAATTGAAAAGACTTTACATCTCAGAAGGTGCCTTGAAGGTCTGCAACTTGAGGTATTGAAACCTTGC
CATGTGAAACCTTGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGGAATCA
TTTATCTGCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGAACGGAAATGCCATTGACAACCTCAGTCACTAGTGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGCATCATCTAGAGCGATACATTACATCACAAACCTTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGCCCCGGTG
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAACATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGTACAAAGTGCAGTAGCTGT
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACGTGCAAGATAAGGCATGTACACATGTATGGTGGTAA
TTCCGGTGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCAAGAACCAACTCTTCTCTTACTTT
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACCACAGATAACAAATGTGGGTCCCACCTC
AGTGGTCAGTGGAGACCAATGTGACCCACTCTCACACCCACAGAGCACAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGAATGATAAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGACTACAAATCATCAT
TGGGTGTTGGCCATCACACTCATGGCTCAGTGTGATGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTGGATGAGGATACGGGAGACACCC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCT
CAACACACAAACAGTTAACACAATAATTCAATACACAGTTCACTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATTAAACATTACAGAGTTACAAAAAACAAACAAATCAAAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAACAA
AAAAGAAAAGAATTATTATTAAATTCTATTGTGATCTAACAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAAACCTCTGTTGAGTTGGCAGTTCTTTCGGTTTCCCTCTGCTGTTGGGGCA
TGAAAGGGCTCGCCGCCGGAGTAAAGAAGGAATTGACCAGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGCACCCCTGGCTGGAAGTTGTGCCGGGCCCGAGCGCGCCGGCTGGAGCTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCGAGCCTCGTGCCGCCGGACTCGGGCAGCCCTCTGGGTAGCGCC
GCGGTGCTGGGCGCGTGGCGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGTAGCGCC
GAGGCCCATGCCCCACTACCTGCCGCTGCCCTGGGACCTGCTGACTGAGTCAGTCAGCGCTAGCGCGTCTT
CCCAGGCCACTCCCCTGCTGGGTGCGTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACAAACAATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCCTGGCTGGAAACAGGATTGTAACATCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATATTCAAGAGCTCCAAACTGCAATTCCAGCCCTACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAATTGGCCAACACA
CTCCTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCCTGGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAACATTG
CAGCTGGACCATAACACCTAACAGAGATTACCAAGGGCTGGCTTACGGCTGCTGATGCTGAGCAACTTCA
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGAGGTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCATCACTTATCAAGGTTAGATGATGTTCAAGCTTCTGGCTTAAGCTTAACTAACATGCAATTGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGCTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGGTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCAATTCAAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAATTTCAGAGCTTGT
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCCAGATGGCTTGT
GATGATTTCCTAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCAATGACTTTGCTGGAAAAAGACAATGAAACTACTGCATGAT
GCTGAAATGAAAATTATGACACACTCCGGGCCAAGGTGGCGAGGTGATGGAGTACCACTCCTGGCTG
CGCAGGGTGAATTGCAAGTGAAGGGAAATACAGTGTGTCATCTCAACTTGGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCACGCTGGAGTGTGCTGCTGTTGGGCCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGCATGTCATGGCCAGGATGACGTGTTCTTATGTTGAGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTGCGGCCACTGTGGACCGAAACTGTAACCAAGGGAGAACAGCCGTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACAAAGATAGCCATTGGTGTAAACCGAGAGGAC
TTTTTGCAAGCAGGAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGTGATGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAACAGTGCACCGCTCAGTGTGATCCCACCTCAACCTGCACTCC
CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCGTGGTTGCTGT
GTGGTGGGACGTCACTCGTGTGGTGTGTCATCATATACCACACAAGCGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTGCCAGCAGATATTCTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCA
GATGGGTACGTGTTCAAGAAAGTGGAGGCCACCCAGTTGTACATCTCAGGTGTGGATTGTTCTTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTC
CTTGTCCGTTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGATCCTTTGAAACA
TATCATAACAGGTTGCACTGCCAGCAAGAACAGTTAATGGACCACTATGAGCCAGTTACATAAAAGAAAAAG
GAGTGTACCCATGTTCTCATCCTCAGAAGAATCTGCGAACGGAGCTTCAGTAATATATGTCGCTTACAT
GTGAGGAAGCTACTAACACTAGTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTCATAACAAAGTCC
TCTTAGATTAGTGCACGAGGCCACCTGAGTCAGTGCCTATTCAAGCTTGGACAGCCATCAGATTGTCAGGCAAGAGCCTTT
GCTCTCAGGAGACCTCAGCTAGATGCTTCAAGCTTGGACAGCCATCAGATTGTCAGGCAAGAGCCTTT
TTGAAAGCTATTCTCCCCAGACTTGGACTCTGGGTCAAGGAGAAGATGGGAAAGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAAAGAAACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGGAAAGCTAACATACTACCTCAAGTGAACCTTTATTAAAGAGAGAGAAT
CTTATGTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAAATTAC
AAAAAGTTATGAAATTCTTATGACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTT
TTTATGCAAAAAGTATCTACGTAATTAATGATATAAAATCATGATTATTTATGATTGTTATAATGCCAGA
TTTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT
ACTCATTATATTGCACTTATATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELQPSCVAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELRNPKIKNDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNEIS
WTIEDMNGAFSGLDKLRLILQGNRIRSITKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPHQQLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLASFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYCTAQNSA
GSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLODDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTLADRQ
DGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFCPFLGSTGPMY
LKGNVYGSDFETYHTGCPDPRTVLMHDHYEPSYIKKECYPCHPSEESCRFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGGGAGAGCGCCAGCTGACTTGAATGGAAGGGAGCCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCTGTGGGCGCCCTGGCGCCGGGGCGCAGCAGGGAGGGGAAGCTGTGGCTGCC
CTGCTCCACGGCGCCACTGGTGTGAAACGGGAGAGCCCCTGGTGGTCCCGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGAGGGCTCATGGTGAGCAAGGAGGCCGGTGTATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGGAGGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGTGTGC
TGCTCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGAGGGCCCAAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCAAGAGAACGAATTGCGGAGGAGGCCGTGTGACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGCGTCAAGTGCCTGGAGACTGTGCTGTTCCAGGAGGGCGTGTGACTGTG
GCGGTATTGACCTGCGTGAGTCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGAGAACAAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAACAAACCAGCCTGA
CTTCCCAGGGCTCCCAGAGAACGGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGACCCCCGCTCCTGCCAACGCCCTGATCAGTGTGGACTTGCTGCCAACTATCTACCAAGATCT
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTACCTGCACAACAAACAAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTCAACGGCTCAGCAACGCTGAGGTCTCATCCTGTCCAGCAACTTCCCTGCCACGTC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAAGCTGAGAACAGATCCCCCGGGGCCT
TCAGCGAGCTGAGCAGCTGCGAGCTACCTGAGAACAAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGGCTGGAGTACCTGGATCTGTCAGCAACACAGCCTGAGGAGACTTGCACCCACTGGCCTTCCAGG
CGCGCAGCCTGGCTGCTGCACTTGGAGAACACGCCATCCGGAGCGTGGACGCAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCAAGCAACAGCTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGC
TCAAGCGGTTGACACCGTGCACCTGTACAACAAACGCGCTGGAGCGTGCCTGGCAGTGGCCTGCCTGCCGCGTGC
GCACCTCATGATCCTGCCAACACAGATCACAGCATTGGCGCGAGACTTGCACCCACTTCTGGAGG
AGCTAACCTCAGTACAACCGCATCACAGCCCACAGGTGCACCGCAGCCTTCCGCAAGCTGCCCTGTC
GCTCGCTGGACTGTGCGGCAACGGCTGCACACGCTGCCACCTGGCTGCCATGGAAATGTCATGTGCTGAAGG
TCAAGCGAATGAGCTGGCTGCCCTGGCACAGGGGGCGTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCGAGCCCTGGGCCCCGTGCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA
TCGCCGGAAATCAGTCACAGAGATCCCCGAGGGCTCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCGGTGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT
TAGAGTTTGGTACATTCCAAGGACCGTGGCGCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAACAAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTTTCTG
AGCACACGCCCTGTGCTGAGCCCCCACTGTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCATGACACGGCTGACACAGTCTCATATCCCCACCCCTGCCACGGCTGCCCCAGGCCAGACACATGC
ACACACATCACACCCCTCAACACCCAGCTGCCACACAAACTACCTCCAAACCCACACAGTCTGTACAC
CCCCACTACCGCTGCCACCCCTGTAATCATGCAGGGAAAGGGCTGCCCTGGCACACACAGGCCACCA
TTCCCATCCCCCTGTCGACATGTGATGCTGATCACACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAGCTATGCCACAGACAGCTTGTCCCCAGCCAGAAATGCCATAGCAGCTGCCGTGCC
GTCCATCTGTCGGTCCGTCCCTGGAGAACACAGGGTATCCATGCTCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATCCTTCCCATCCTATGGGGACAGGAGGCCCTCAGGACTGCTGCCCTGGC
TGGCCACCCCTGCTCCCTCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCGCCACGCCCTGGCAGGACA
CAGGCACTTTCAATGGCAAGCCAGTGGAGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGCCTTGGG
CAGGAGTGAAGCAGAGGGTGTGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTTCAGGCCTGTGGGGAGTTCCGGTGCCTTATTTTTATTCTTCTAAGGAAAAAAATGATAAAAT
CTAAAGCTGATTTCTGTTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFFEHTNLNYLYLANNK
LT LAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RVR TLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLK GIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCCCGCAGCAGACCTGCTCCGGCCGCGCCTGCCGCTGTCCCTCCGGAGCGGCAG
CAGTAGCCCGGGCGGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGGCCCTCCCATCGCGCCACCACCC
CAACCTGTTCTCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTTCCTCTGGCTGGT
GCTGGTATCTCGCTCACCTGAGGGGCCGAGTTGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGCTGTTGGGGAGGATGACTGCTGCTGGGGCTGGGCTGCCAGTCTTGGGACAGTGTAGCC
TGTGTGCCAACACGATGAAACATGGTAATGTATCGGGCAAACAAGTGAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGATGAAACACTTA
CGGCAGCTACAAGTGTACTGTCTCACGGATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCACTGGCTGTGATGTTAAAGGACAATACGGTGCAGTGCCTGCCATCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTTGAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTCACAACTTTGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTTATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGTCACTGGTCAGTCACTGTCAGCAGCAGCTTGCTGATGTTATAA
CGTACGGGCTCTACAAGTCAAATGTAAGAAGGATACCCAGGGTATGGACTGACTTGTGTTATGCCAAA
AGTTATGATTGAAACCTTCAGGTCACATGTCACCAAGGGAAATGGTACATTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGAAAGTACTGGCTCCGAAGACACCATATTCTCTCATTCATTACCAA
CAGGCCACTTCTAACCAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCAACCCACCAACCC
CTGCCAACAGAGCTCAGAACACCTCTACCAACCTACACCCAGAAAGGCCAACCAACGGACTGACAACATATAGC
ACCAGCTGCCAGTACACCTCAGGAGGGATTACAGTTGACACAGGGTACAGACAGACCCCTAGAAACCCAGGAGG
AGATGTTGTCAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTCGACTGGAAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCAGG
GGGAAAGCTGCACGCTGGTGTACCTCTCGGCCGCTCATGCATTAGGGACTGTGCCGTGATTAGGCA
CAAGGTGACGGGGCTGCACTTGGCACACTCCAGGTGTTGAGAAAACACGGTGCCTACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTTGGCAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAACCATGATGGTTTCAAGTATATGAGGGTGGCACAGAGAGGGTGGCAGCAG
TTCTCCATATGCACTAAGAATAGAACAGAGGAACGGCTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTTCTAAAGGAAATTAGA
AAAAAATTGTCATTTAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCCAAA
AGATGTTTGATCTACTAGTAGTATGCACTGAGAAAATCTTAGAACTAAATTGGACAAGGCTTAATTAGG
CATTTCCCTCTGACCTCTAACGGAGGGATTGAAAGGGAGGCCACCAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAACTCTAGCAGTATTAAGAAAAGGAAACTATTCTCAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAAATGCTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTCTATTGTCATGGGATGTTGAGGTTCAAGATTTTTTTAAGAGATCTTCAAGGAAACACAGTTCAGAGAG
ATTTTCATGGGTGCACTCTCTGCTGTCAGAAGGTTATCTGGCTGCTGAGAAAAGAGTGCCTGGCCCC
ACACCGGCAGACCTTCTTCACCTCATCAGTATGATTGAGGTTCTCTTATCAATTGGACTCTCCAGGGTCCAC
AGAACAGTAATATTGGAAACAATAGGTACAATAGAAGGTTCTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAGCCTTGGTACAGGCGAGAATATGGCTGAGATCCATTGTTAATGGTTATT
TCCCTTATGGTCATATAACTGCAAGCTGAGATGAAAGGGAAAATAATGAAATTGTTACTTTCTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAAATGTTT
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAACAATTATTGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYI GGGKYQCHD IDECSLGQYQCSSFARCYNVRGSYKCKC
KEGYQGDGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA
AASTPPGGITVDNRVQTDPQKPRGDVFSLVHSCNFDHGLCGWI
REKDNDLHWEPIRD PAGGQYLT
VSAAKAPGGKAARLVLPLGRLMHSGDLCLSFRHKVTGLHS
GTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA
ACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGAACTCTATGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTCAGATTCATCCTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTAGGAACCTGTCAGTGAATGAAAGTGATATCATTATGCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCTTCTCTTCTATGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGAATATATGAATTGTTCTCAGATGTTCTGGTGTTCAGG
ATTCGAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAG**TGA**ACTTCTGG
GCTAAACAGTACATTCAAGTGAAATTCTGAAGAAACATTAAAGGAAAACAGTGAAAGT
ATATTAAATCTGGAATCACTGAAGAAACCAGGACCAACACCTCTACTCATTATTCTTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTCAAGTTTATTCCAAATTCTATCTTGTATTGTACAA
TTAAGAATGCTAAATTATGTTCAATTCTTCAAGTTTATTAAATTATTAGTG
CAAAGTAATAAGGATGGTTGTACAAAAACAAACTATGCCCTCTCTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPHPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGC~~AA~~**A**TGGCGCCCTCCGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCTCCCTGGACGCACGGCGGCGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCACTATTTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGACTGTTATTAGGACTCTGTATGATATTGTGTC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC
CATAAAGACAAACGCTCTGGTCCATCATTGCCACAGATAAATCCT**AG**TAAATTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCACTGATGTTATTGATTAAGAGACTA
CATTCAAGACATAAAAGCACTAGGTATAAGTTGAAATATGATTTAACAGCACAGTATGATG
GTTAAATAGTTCTCTAATTGAAAAATCGTCCAAGCAATAAGATTATGATATTGTT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCATTAT
TGAGGTATTAAAGAAGATTATTAGAGAAAATATTCTCATTTGATATAATTGTTCTG
TTCACTGTTGAAAAAAAGAAGATATTCCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTTCAGTGACAATTCTGGTCTTTAGAGGTATTCCAAAATTCTCTG
ATTAGTTAGGTTATGCAACTAAACACTACCTTACATTAATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCACTGGTATTCTCTGATT
CAACAAAGTTGATTCTCTGTATTCTACTATGGTTACATTTTATT
CAAATTGGATGATAATTCTGGAAACATTGTTATGTTTAGAAACAGTATTGTT
GTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATTAAATT
TTGCCACTTTTCAGATTTCATCATTCTGCTGAATTCAACTTGAAATTGTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTGCTGTGATGTGAAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTCTGTATATGCTTAAATGTATTGTCCTCATACAGAAAGTTCTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATTAAAAGACAA
ACTCATATTATCCTGTGTTCTTCTGACTGGTAATTGTTGGGATTCACAGGTAAA
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTAAAGAGCTAGAATACTAGTTT
CACCTTAAAGAAGGGGAAATCAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCTCTTCTAGGCTCTGCTGTGAATTGATTAGATTACAG
TATCGTAATATAAGTTCTTAAAGCCCTCTCTTAGAATTAAATATTGTACCA
AAAGAGTTGGATGTGTAATTGATGCCTTAGAAAAATACCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCAGGCGATTGGAAGAGCGGG
AAGGTCTGGCCAGAGCAGTGTGACACTTCCTCTGTGACC**ATGAA**ACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGAGGCCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTACCCGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCAGCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGGCTCACCGCCGCTGCTC
TCCCTTGACCCAACGCCACGAACGAGCTGGAGGGAATCTCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACGAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG
GAGGGTGTCAAACGTACACCCCCGTAGACAGAAAGAGGCTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCTCAAAGAGGAGGAGCTGGGACAGCCCGACA
TCGTCAGGTACTACGATGTATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGAAAAA
CCTAAACTTGACGCCACCGTCTGATCCAAAGACAGGAGCTCCTACTGCGCCAGCTA
CCGGGTTCCAAAAGCTCCTGGTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTGTACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAACAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTGTGGATCAACAGAAGTTGACT**TG**A~~C~~ATCCTTCTGTCTTCCCTGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCATTCAAGCCTGCCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATGTCCTACAGAAAAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHHGNRAPQOLLIAPFKEEDEWDSPHIIVRYYDVMSDDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTGGCTGGGGTAGTCCGACACCTCACAGTTGAAGAGCAGGCCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGGATGCTGGCTCTGGAAAGCAGCGGGCTTGCTCTGTCTTGGCCTCATGACCC
CAGGTTCTCTGGTAAAACGTAAAGCCTACTAGGCCTGGTGCCTCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGCAGGGCCTACCAACCATGCGACTGAGCTCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTAGGGCTGCTCTGGGTGCAGCCTGAGCCTCTGCCGGTTCTGGATCCAGGGGAGGGAGAAAG
ATCCCTGTGAGGCTAGGGGAGCAGGAGGGCCACAGAATCCAGATTGAGAGCTGGCTAGACCAAAGTG
ATGAAGACTTAAACCCGGATTGCCCCACTACAGGGACCCCAACAAGCCCTACAAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCGTGAGCGGTTGCTGGCTGTGACCTCCCAGCTACACTGTCCA
CTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGTTACTCTACTTCACGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGGCGACTACGACTGGTCTTCATCATGCAGGATGACACATATGTGAGGCC
CCGCCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATG
GCGAGCGAGCAGGCCGGTACTGTCATGGGGCTTGGTACCTGTTGTCAGGAGTCTCTGCTCGTCTGC
GGCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGGCTCTGACGAGTGGCTGGACGCTGCCATTG
ACTCTCTGGCGCTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACTGGCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGTTCTGAGTGCCTCGCCGTGACCCCTGTCAGGAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTGGAGCGGGTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCTGGCTCCCTGCTCCTTCA
CACCAACTCTCGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACCTCTCCTGTGAGATGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGGAGCTGGAGTGGCTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCCCTTCAAGACAGCAGACTGCTCAACGGCTATGGCGCTTCGACCCAGCAC
GGGCATGGAGTACACCTGGACCTGTTGGAATGTTGACACAGCGTGGCACCGGGCCCTGGCTCGA
GGTCAGCCTGCGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGGCTTGCAGCCAATGTC
TGGAGCCACGAGAACATGCAATTGCTCACCTGTTGCTGGCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGCGTACCCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCAGACTCATGGACGTGGCTCGAAGAACGACCCCTGTGGACACTCT
TCTCCTTACCAACCGTGTGGACAAGGCCTGGGCCAGTCTCAACCGCTGCGCATGAATGCCATCTCTGGCT
GGCAGGCCCTTTCCAGTCCATTCCAGGAGTTAACCTGCCCTGTCACACAGAGATCACCCCAAGGGCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTTCTGCGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCCCTAACCTATTACCTTCTGTGCTCAGCC
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGCCCTAACCTATTACCTTCTGTGCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAACATTGTTGCTGTATTAAATGAAATGTTATTAA
ACATGTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGPQNPDSSRARLD
QSDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLVYGPREGGRGAPDPFLGVKAAAAELEERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCCGTGCGCGCTGC~~G~~CTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACAAACACTGTGACAAAGCAG
AGTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA~~ACT~~G
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAAGATGCTGATGG
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTTAGATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTAGGCATTGGCATATTTCAT
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTTAGTAGTAACATACATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTCTTAAACACATGAACATTGAAAT
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGGAAAAT

FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGTGGCCCCCTCAGCAACCTCGACATGGCCTGAGGGGGCCACCGCAG
TCCGGCTCTGCGCTCGGCTGCCGTACTCTTCCTGCTGCTGCTTTCAAGGGGCTGCCGTATAAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGAAACTGTCTGCATCATTACGGATTGCG
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGGGCTGTGCAGAAAATCTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTAGGTGCTCGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCAGGCTGACCGTAGGCAAGATGCCAACACTGC
ACTGCCAGGAGAGTGAGGGCACCCCCGGCCTACTACAGCTGGTATCGCAATGATGTACCAACTGCCAACGGATT
CCAGAGCCAATCCAGATTTCGCAATTCTCTTCACTTAAACTCTGAAACAGGCACCTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGGAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGCTCTGCTGACTGGCCCTGA
TCACGTTGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTTCAGACACAAAGTCACTGTTG
TGATCTGAGACCCCGGGTGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCTGTC
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGGCTTTCTGTTGGCCAAGGTGACCA
CTACTCTTCTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATAATAACCACAA
GGAAGCGAAACTGGTGGCTCACTGAGTTGGTCTCTTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGGGCTGTGAAGGCCAGCATGTTACCAACTGGCTGTT
CAGCAGGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAAACCC
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCAACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTGTAAAAACAACCAAAATCAGGAAG
GTAATTGGTGTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCCAACAGGGTGTAGGATTTAAGGAAA
ACCTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAACTGAAATATATTG
TACATCTAAATTGGTCAAGGATGTTGATATTGAAAGAAAATTCTATTAAACTGAAATATATTG
CATACAATGTTAAATAACCTATTGTTAAAAAGGTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAAGGTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTAGCCTTTCAAGGGAACTCATACTGTCACACATCAGACCAGTTGCTTAGGAAACCTT
AAAAATTCCAGTTAGCAATGTTGAAATCAGTTGCTCATCTTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTCACACAGATG
CCAGTCAGCTCTGGGTTGCCAGGGCCCCCTCTAGCTCACTGTTGCCCTGCTGCTGCCAGGAGGCC
GCCATCCTGGGCCCTGGCAGTGGCTGTCAGTGGCTTACTCACGTGGCCCTTGCTTCACTCAGCAGC
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTTCCATGTTAGCGTCCCAGCTTGGGCCCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTTAAGTTGTTAATTATTGTT
AAGATTGTCTAAGGCCAAGGCAATTGCGAAATCAAGTCTGTCAGTAACTTAAACATTTTAAAGAAAATGGAT
CCCACTGTTCTCTTGTGCCACAGAGAAAGCACCAGACGCCACAGGCTCTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGGGAGGAAAG
TGAAACGCCGTAACAAAGCAGTTCTAATTGACTTTCAATTGAAACACTTGCCTGAGGAGCAGGTGTTCTCAGC
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCAGATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCAGTCCACTGTC
GAATGGCTCTACTACTCACCTTGTCTTCAAGCTTCAAGAGCAGGTGTTCTCAGCCTCAGATGCC
AATTGCATACATGAGACTGTGTTGACTTTTGTGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGTCAGGATGCTTAGCATGCAAGTT
CCTCCATATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCCTGGGATTCA
CTCTGGTGTCAAGTGTAGGGTAGGCCATTGGCCCCCTTCTTACACCTAAACCTTCAACTAGTGC
TGGGAACCAAGGCTGAAAAAGTAGAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCC
CGGAAAAGGAATACTCGTGTTAAGATGAAATGTGACTCAAGACTCGAGGCCGATAC
CGGAGGCTGTGATTCTCATTGATGGCATTTAAAGCTTCAAAACCC
CTCATTATAAAAGCTTCAAAACCC

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFFFRLRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAVRGGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267